

Fig. 1

2/16

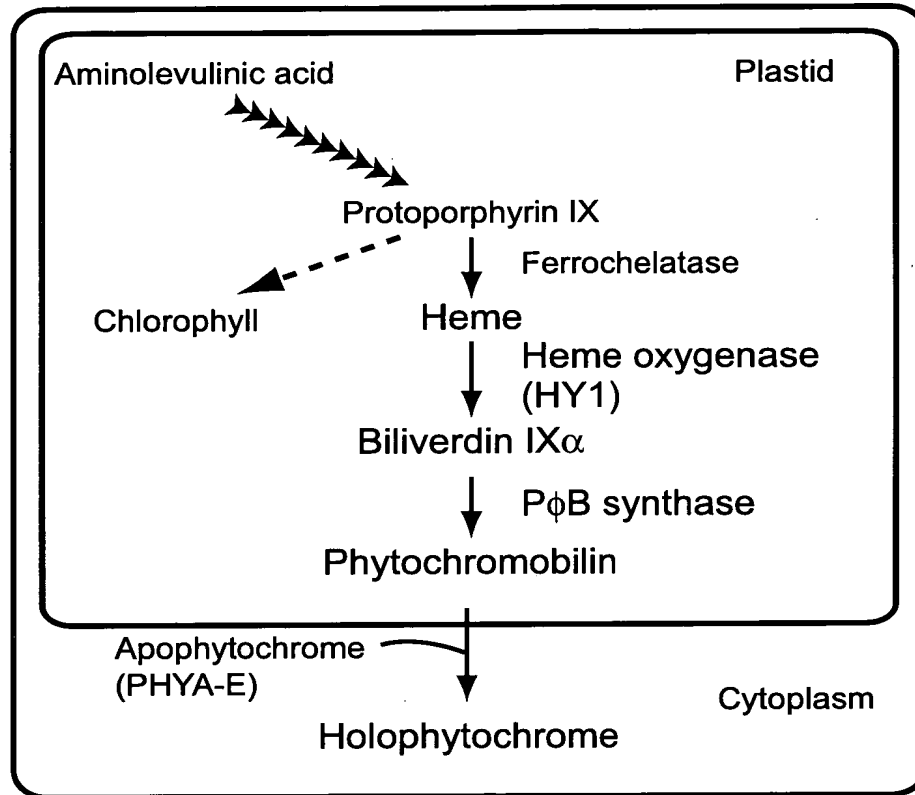
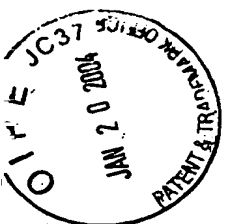


Fig. 2



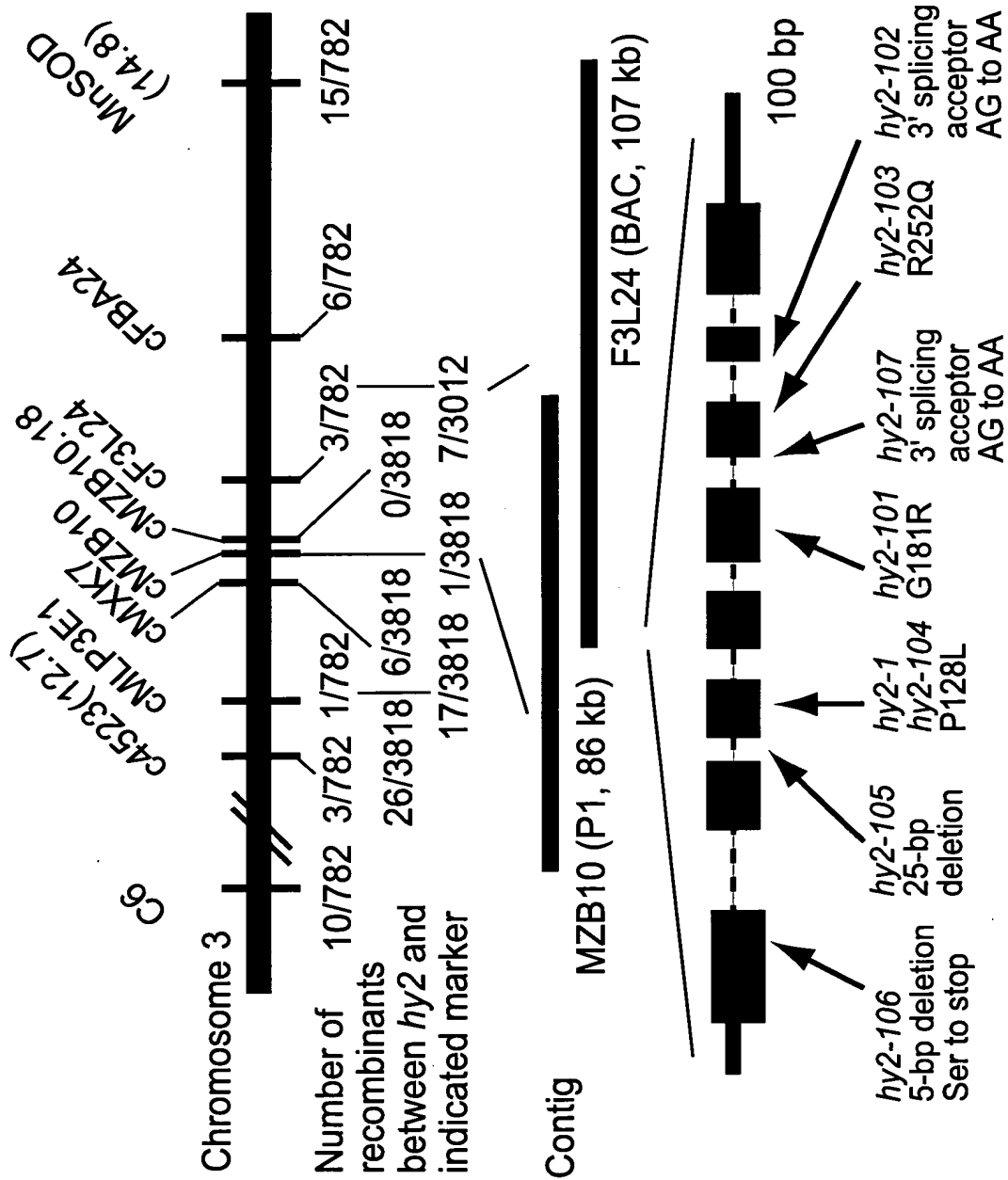
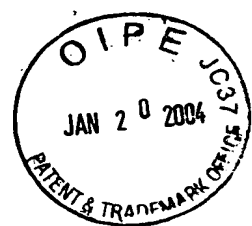


Fig. 3A



4/16

gaattccccacgtcaacgtgactgtgcattccacgtggcggtatgtggccctatagttgg 60
aocattgactcggacggatgttgaattcattgtcgttgccaattgcgtttgtctcactga 120
aactgtgaaattttatctcttttatagataaAGAATCTTGCTTTTTCAGTTTTCAGTA 180
TGAAGAAGAATTGAAGAGAGTGTCCGAGGAAGGAGACCTTTGGTTTCAGTTTGTGAGTCT 240
TGTGTGAATGGCTTTATCAATGGAGTTTGGGTTTTCATTTGGGTCATGCTTCAAGGCACC 300
H A L S M E F G F S I G S C F K A P
AAACCCACCTGTTCTAATCTCTGCAAGCCCTAATAAGATCAATTTACGTTGAGAAGGAG 360
N P P V L I S A S P N K I N F T L R R R
AAAGAAAAGATTCTTACTTAGAGTCTCTGCTGTGTGCTATAAGGAATTCGCAGAGTCTGC 420
hy2-106 *****
K K R F L L R V S A V S Y K E F A E S A
TTTAGAAGAAACCAGGAAAAGGATCGTTCTTGAACCTTCACATCTCCAGgtatatgcaat 480
L E E T R K R I V L E P S H L Q
taccatttggttagttagtggaggatttatattctcattgtttcttgctgtgaattttg 540
ggttaattgatttgagttgtcattaggaacaaacaaataactttactgttatagactgc 600
ttatataagtaaaagttcagattttgtttttctaatcacgaactgtttcagGAAAAGTA 660
E K Y
TAGTAGCATGACAGGACTAGATGGTAAGACCGAACTTCAAAATGCTTGCTTTTAAATCTTC 720
S S M T G L D G K T E L Q M L A F K S S
AAAGATTAGACTCTTGAGGAGTAGGCAATAGAGAATGAGACAATGCAGgtttaacttca 780
K I R L L R S M A I E N E T M Q
gcagtacaaactgattgttttagtccatttcocttactttcaattgattgattgtttgta 840
hy2-105 *****
tcttgcgttagGTCTTTGACTTTGCGGGTTTCATGGAGCCTGAGTATGATACTCCCATAT 900
hy2-1, hy2-106 T
V F D F A G F M E P E Y D T P I F
TCTGTGCTAACTTTTTCACATCTACCAACGTTAACATAGTTGTATTgtaagtatatcttct 960
C A N F F T S T N V N I V V L
agttatgctggagttatcaggctctgtattgtccaaactgatgttcaatattttactgtat 1020
gttctctcttagGGACCTTAATCCTTTGCATCAGTTGACTGACCAGCGGATTACCAAGA 1080
D L N P L H Q L T D Q T D Y Q D
CAAGTATTATAACAAGATAATGTCCATATATCACAAATATGCTGAGgtgaccacaagaat 1140
R Y Y N K I M S I Y H K Y A E
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atttatttgacagACTTTCCCATGGGGAGGGAAATGACTGGTGAATCCATAAAGTTTTC 1260
hy2-101 A
T F P W G G K L T G E S I K F F
TCGCCTTTGGTGATGTGGACTAGGTTTTCGTCTAGCAAAGAAAAACATAAGGCTTTGTTT 1320
S P L V M W T R F S S S K E K E K A L F
TCTGCGTTTCTAGAGTACTATCAGgtatatactcagcgcccaaaagctaagggttttattg 1380
S A F L E Y Y Q
gaaactttgactgagaatctatcatcttcttctacagGCATGGCTTGAGATGACAATCC 1440
hy2-107 a
A W L E M T I Q
AAGTGAGGGAGGAGATGGAACCATCTCATGTGAGAGCCAAATGTGAAGCACAACACAAGT 1500
V R E E M E P S H V R A N C E A Q E K Y
ACCTGACATGGCGAGCACAAAAGgtgatttcatttcoctttgtgtaatttgcatgtttga 1560
hy2-103 A
L T W R A Q K
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hy2-102 a
D P G
CATGGTCTTCTTAAAGATTAGTAGGTGAAGCAAAGGCAAAGgtatataaaagatttgatoc 1680
H G L L K R L V G E A K A K
cattagtgccccattattaattagcttgtgaagatgttgaaaatgatttgaacaaaatc 1740

Fig. 3B

5/16

1.35 kb

hy3-107

WS

hy2-106

hy2-1

Ler

hy2-101

hy2-104

hy2-103

hy2-105

Col

Fig. 4A

rRNA

Fig. 4B

HY2 ARATH : MALSMEFGFSIGCFKAPNPPVLIASPNKINFTLRRRKKRRFLRVSASVKEYFAESALETTRKRIVLEFSSHTQEKYSSMTGLDGK- : 80
YCP2_SYNPY : -----SVIDQSWLMDVPGFERKRWVTRDAGDSLOVFNNAVAYPDYNDHPLMGVDLTFWFGARQKLVAVDFQBLVQ- : 60
YHP2_PROMA : -----TVIKSNLMDVPGFERKRWVTRDAGDSLOVFNNAVAYPDYNDHPLMGVDLTFWFGARQKLVAVDFQBLVQ- : 160
YHP3_PROMA : RNPVHTTTLTAAKFEKI KOVRLACIKGCESSVFNLIHPLNDYDLPFFGADFTLPGN- HMLADLQDRAIKL- DNIHTENVMP : 115
YCP3_SYNPY : SKSIPVTTATWACKTEKEROVRAACVSAGSAA SVLFNPKSTYGLPFFGGDLVTFPAG- HMLADLQDRAIKL- DEVHTTHVWD : 137
SLR0116 : -K- --LVJENRCYQTPQPEKMHIELAKVCKGDIHLHCVMPEPEPLYGLPLEGCDIVAGPGG-VSAATADLSEPTQS- --DRQLPAAAYOK : 135
* 100 * 120 * 140 * 160 *
TELQMLAEKSSKIRLIRSMATEN-ETMOVFDFAGEMEPEYDTPLECANFEFTSTNVN- HVVLDLNLHQLTDQTDYQDKVYN : 165
YCP2_SYNPY : -----SVIDQSWLMDVPGFERKRWVTRDAGDSLOVFNNAVAYPDYNDHPLMGVDLTFWFGARQKLVAVDFQBLVQ- : 115
YHP2_PROMA : -----TVIKSNLMDVPGFERKRWVTRDAGDSLOVFNNAVAYPDYNDHPLMGVDLTFWFGARQKLVAVDFQBLVQ- : 119
YHP3_PROMA : RNPVHTTTLTAAKFEKI KOVRLACIKGCESSVFNLIHPLNDYDLPFFGADFTLPGN- HMLADLQDRAIKL- DNIHTENVMP : 137
YCP3_SYNPY : SKSIPVTTATWACKTEKEROVRAACVSAGSAA SVLFNPKSTYGLPFFGGDLVTFPAG- HMLADLQDRAIKL- DEVHTTHVWD : 137
SLR0116 : -K- --LVJENRCYQTPQPEKMHIELAKVCKGDIHLHCVMPEPEPLYGLPLEGCDIVAGPGG-VSAATADLSEPTQS- --DRQLPAAAYOK : 135
* 180 * 200 * 220 * 240 * 260
KIM- --SYHKKYAEFTFWGCKLTGESIKFTSPLVMTFR- --FSKSEKHKALFSALEYYQALLETIOVREEMEPESHVRANCEA : 244
YCP2_SYNPY : GFK- --EINQREPDINGEETMRSFDPNQVSSWLLFCR- --GGAEQADLSIPKAFSALEKAYWDLHDNAKSPSTIPPEEVKNL : 193
YHP2_PROMA : DLO- --ITKNRRVDFNSQKTMKIYDSNRKPFSEWVLLYN- --GSFDDQLQCSIAKILDEFELHAYWQVNNNSRREYIKIIPSKVQNL : 197
YHP3_PROMA : RMI- --PHDHMQSLLP SGGEIPKEAEPYPSGFLMSRLPLSKESDNIISEIMRPNFEGEXLSLYIELHLAKPKPKKER-ALKILEG : 219
YCP3_SYNPY : RMI- --PHDHMQSLLP SGGEIPKEAEPYPSGFLMSRLPLSKESDNIISEIMRPNFEGEXLSLYIELHLAKPKPKKER-ALKILEG : 219
SLR0116 : SLAELGQPEFEQORELPFWG- --EIESEYCLFIR- --PENVTEERFVQVRVVDLQIHCHQSIVAEFSEAQ-TLEHRQG : 208
* 280 * 300 * 320 * 340
CHKYLTWRAQKDBGHGELRRLVCEAKAKELTRDFLNGVDELGKTKTFIDYFPEYQTEDGTVSDKRSIIGKSYETRPWDLTGQFIG : 329
YCP2_SYNPY : QDKYDIYSAERDPAHGLFTSHFCKDTSNRELHEFLFPASSHK- -- -- -- -- -- : 236
YHP2_PROMA : HINXDIYSAERDPAHGLFTSHFCKDTSNRELHEFLFPASSHK- -- -- -- -- -- : 241
YHP3_PROMA : QKAYINRSTKDDPARALCERFKGKENTEDHKKVLFNI- -- -- -- -- -- : 257
YCP3_SYNPY : QKAYINRSTKDDPARALCERFKGKENTEDHKKVLFNI- -- -- -- -- -- : 257
SLR0116 : QIHYCQQQQKNDKTRRVLEKAECEACERMSQVLEDDVIO- -- -- -- -- -- : 248
q Y Dp G W 6 Lf

Fig. 5

7/16

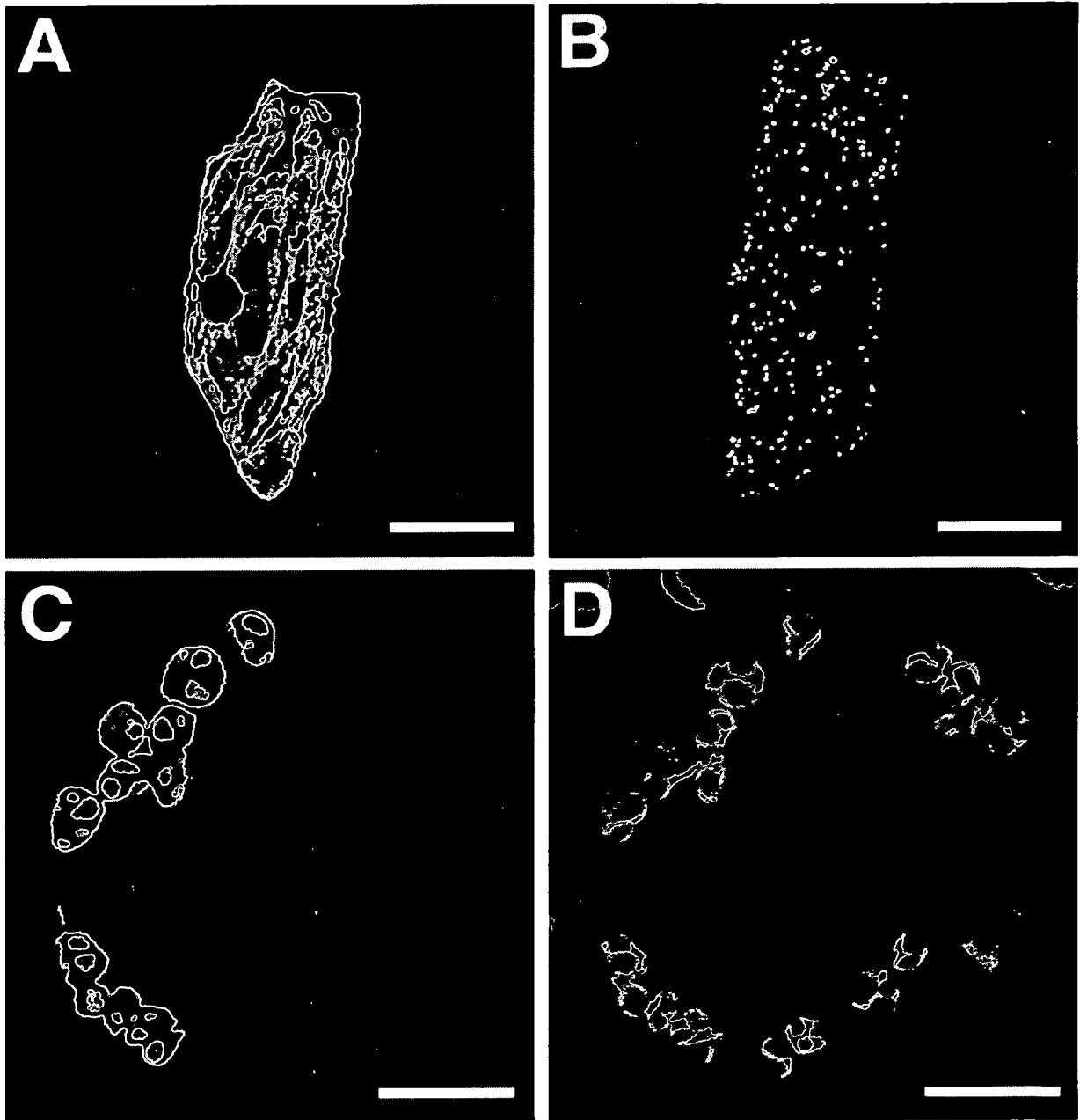


Fig. 6

8/16

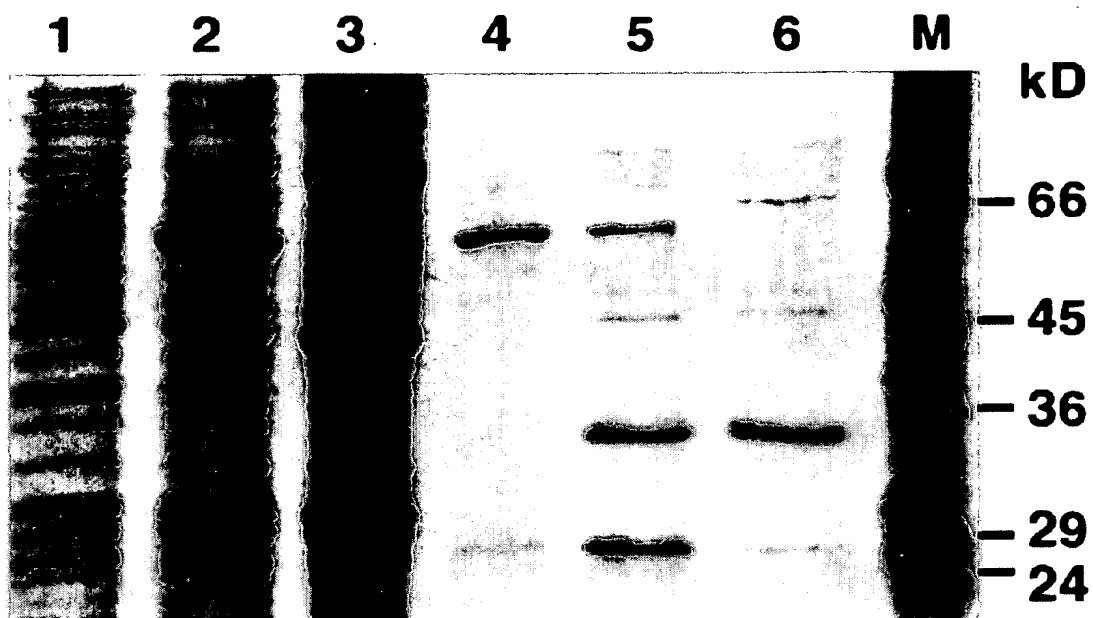


Fig. 7

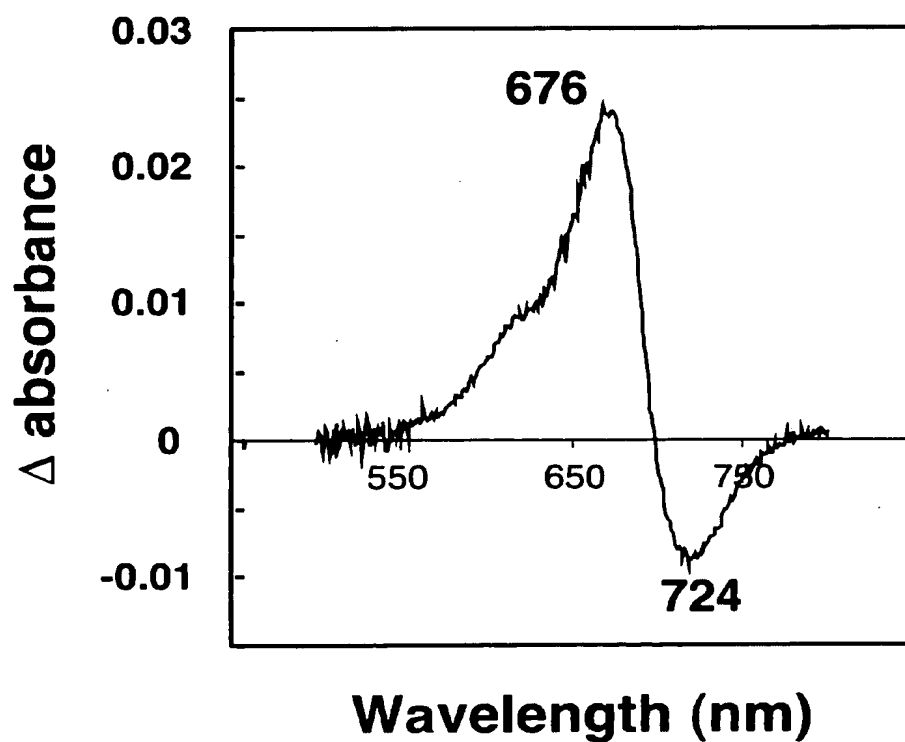


Fig. 8

9/16

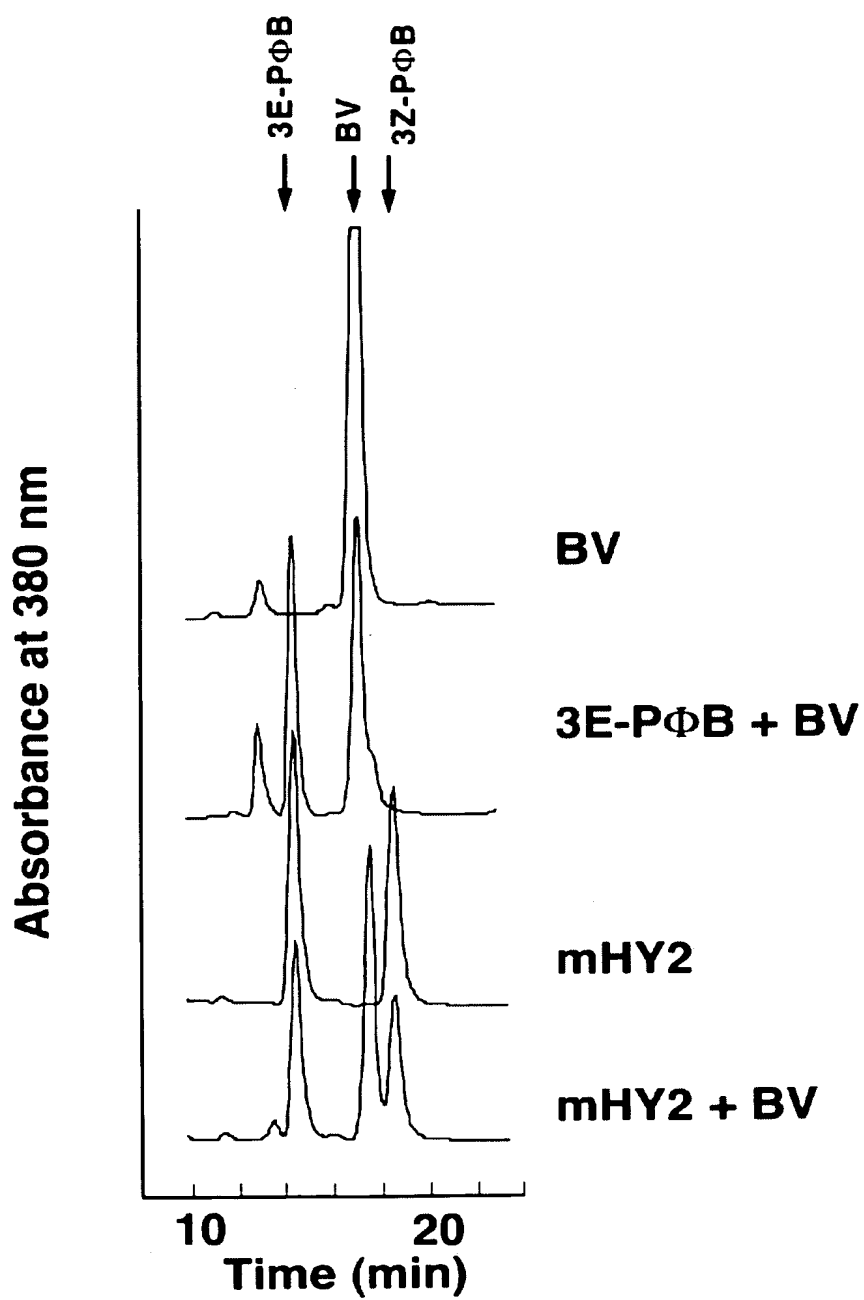


Fig. 9

10/16

[illegible]

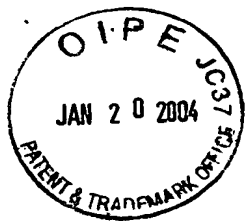
Fig. 10A

11/16

P-ya_ANAS?	260	240	220	200	180	160	140	120	100	80	60	40	20	0
P-ya_NOSPU	199	179	159	139	119	99	79	59	39	19	-1	-21	-41	-61
P-ya_SYNB1	202	182	162	142	122	102	82	62	42	22	2	-18	-38	-58
P-ya_SYNB1	198	178	158	138	118	98	78	58	38	18	-2	-22	-42	-62
P-ya_PRONE	193	173	153	133	113	93	73	53	33	13	-7	-27	-47	-67
P-da_SYNB1	186	166	146	126	106	86	66	46	26	6	-14	-34	-54	-74
P-da_SYNB1	186	166	146	126	106	86	66	46	26	6	-14	-34	-54	-74
P-da_PROVA	190	170	150	130	110	90	70	50	30	10	-10	-30	-50	-70
P-da_PRONE	185	165	145	125	105	85	65	45	25	5	-15	-35	-55	-75
P-da_NOSPU	224	204	184	164	144	124	104	84	64	44	24	4	-16	-36
P-bb_SYNB1	213	193	173	153	133	113	93	73	53	33	13	-7	-27	-47
P-bb_SYNB1	214	194	174	154	134	114	94	74	54	34	14	-6	-26	-46
P-bb_PROMA	213	193	173	153	133	113	93	73	53	33	13	-7	-27	-47
P-bb_PROME	213	193	173	153	133	113	93	73	53	33	13	-7	-27	-47
P-bb_NOSPU	209	189	169	149	129	109	89	69	49	29	9	-19	-39	-59
H2_ARATH	202	182	162	142	122	102	82	62	42	22	2	-18	-38	-58
RCE_ARATH	237	217	197	177	157	137	117	97	77	57	37	17	-13	-33
RCE_HORVU	271	251	231	211	191	171	151	131	111	91	71	51	31	11
	155	135	115	95	75	55	35	15	-5	-25	-45	-65	-85	-105

P-ya_ANAS?	360	340	320	300	280	260	240	220	200	180	160	140	120	100
P-ya_NOSPU	245	225	205	185	165	145	125	105	85	65	45	25	5	-15
P-ya_SYNB1	245	225	205	185	165	145	125	105	85	65	45	25	5	-15
P-ya_SYNB1	247	227	207	187	167	147	127	107	87	67	47	27	7	-17
P-ya_PROME	243	223	203	183	163	143	123	103	83	63	43	23	3	-13
P-da_SYNB1	236	216	196	176	156	136	116	96	76	56	36	16	-4	-24
P-da_PROMA	235	215	195	175	155	135	115	95	75	55	35	15	-5	-25
P-da_PROME	241	221	201	181	161	141	121	101	81	61	41	21	1	-19
P-bb_NOSPU	236	216	196	176	156	136	116	96	76	56	36	16	-4	-24
P-bb_SYNB1	280	260	240	220	200	180	160	140	120	100	80	60	40	20
P-bb_PROMA	257	237	217	197	177	157	137	117	97	77	57	37	17	-13
P-bb_PROME	257	237	217	197	177	157	137	117	97	77	57	37	17	-13
P-bb_NOSPU	257	237	217	197	177	157	137	117	97	77	57	37	17	-13
H2_ARATH	329	309	289	269	249	229	209	189	169	149	129	109	89	69
RCE_ARATH	319	299	279	259	239	219	199	179	159	139	119	99	79	59
RCE_HORVU	205	185	165	145	125	105	85	65	45	25	5	-15	-35	-55

Fig. 10B



12/16

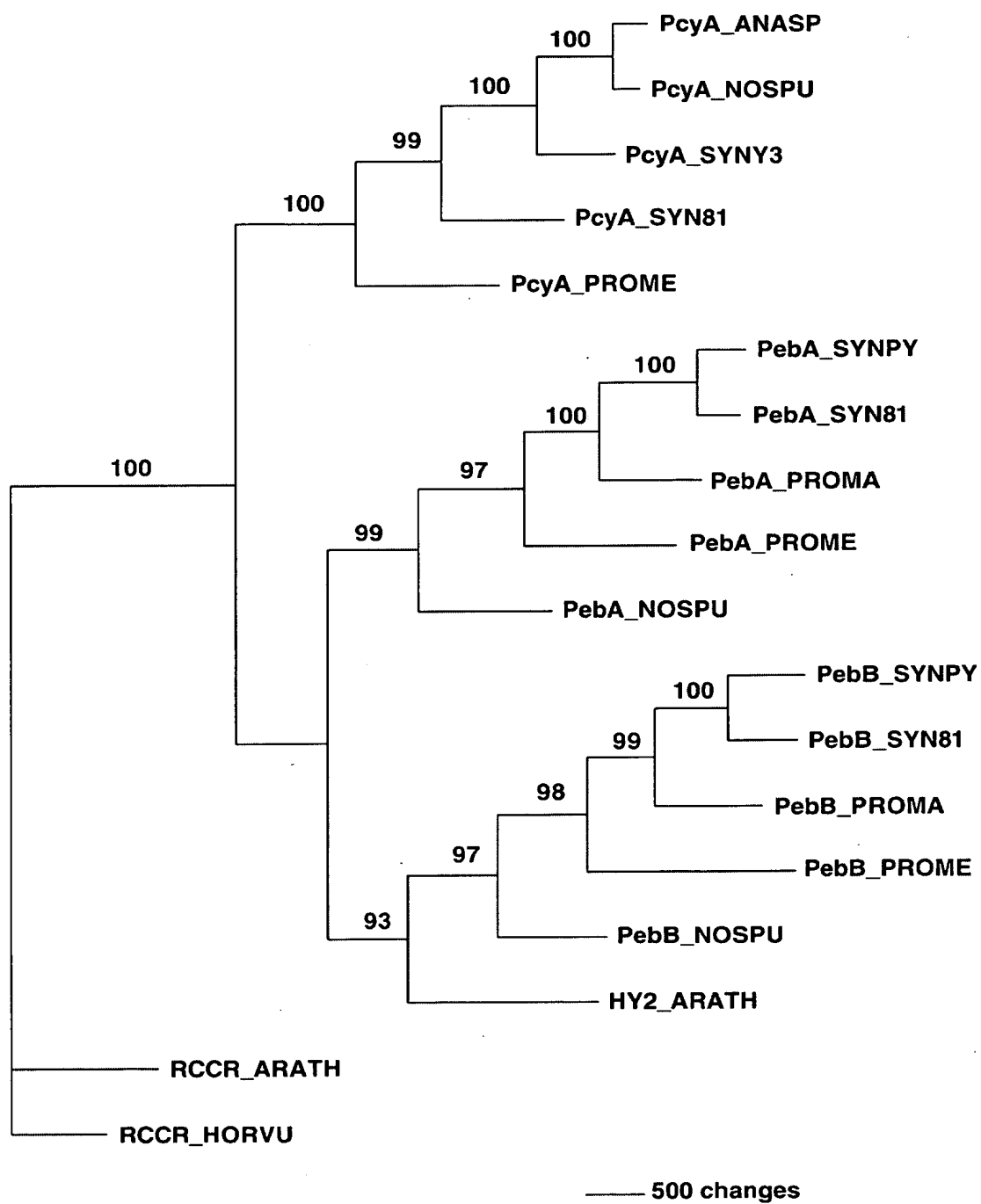


Fig. 11

13/16

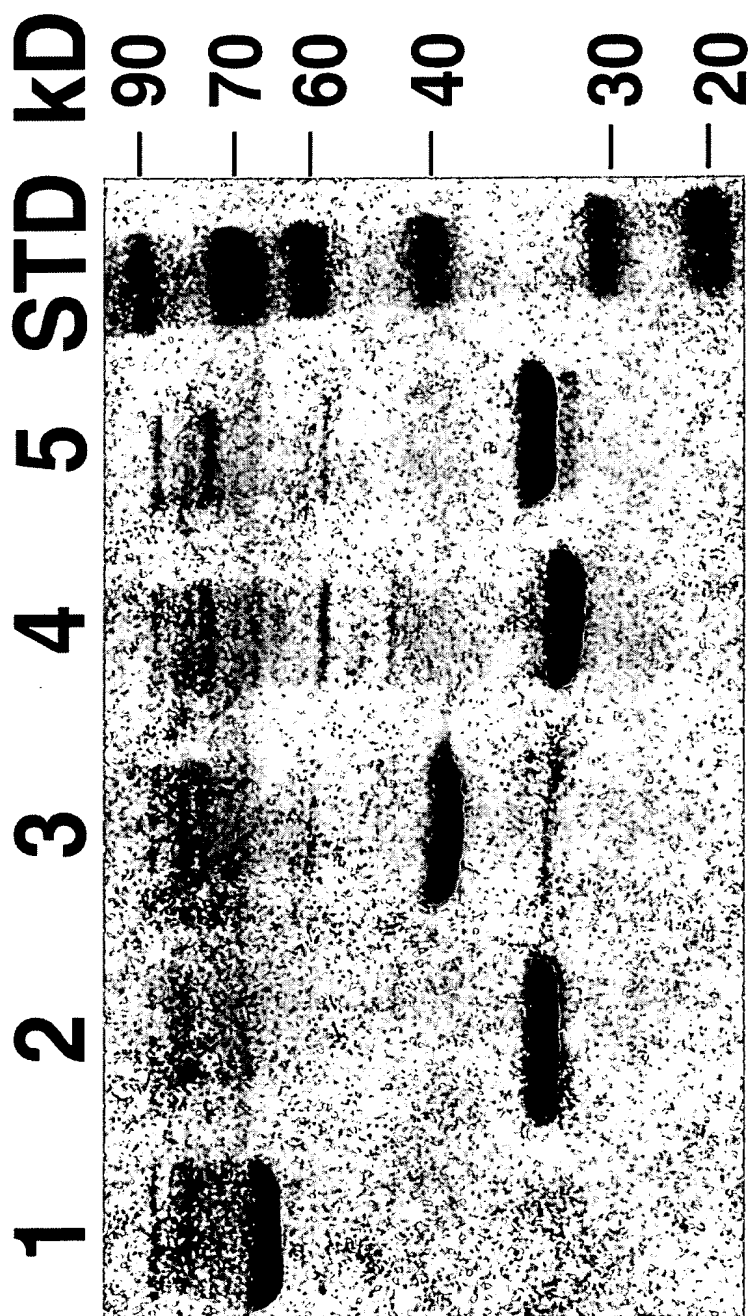


Fig. 12



14/16

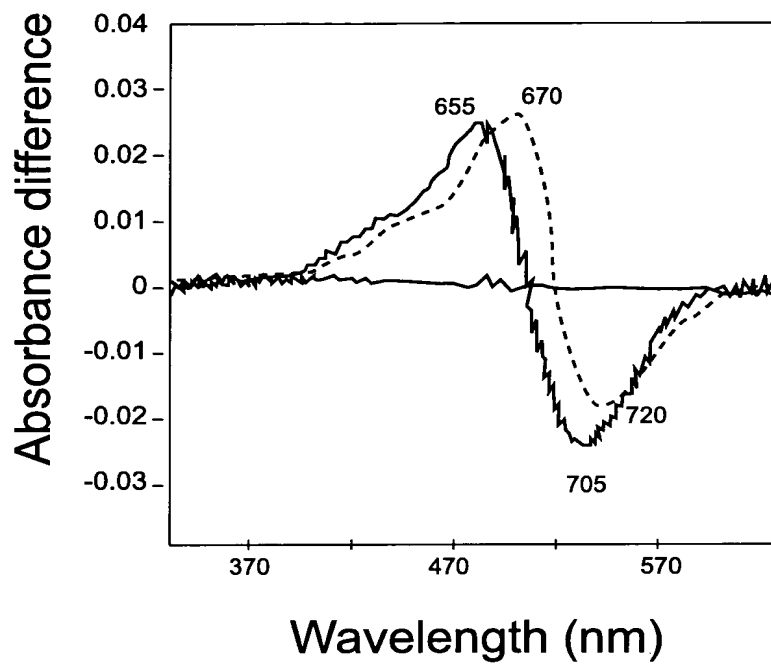


Fig. 13A

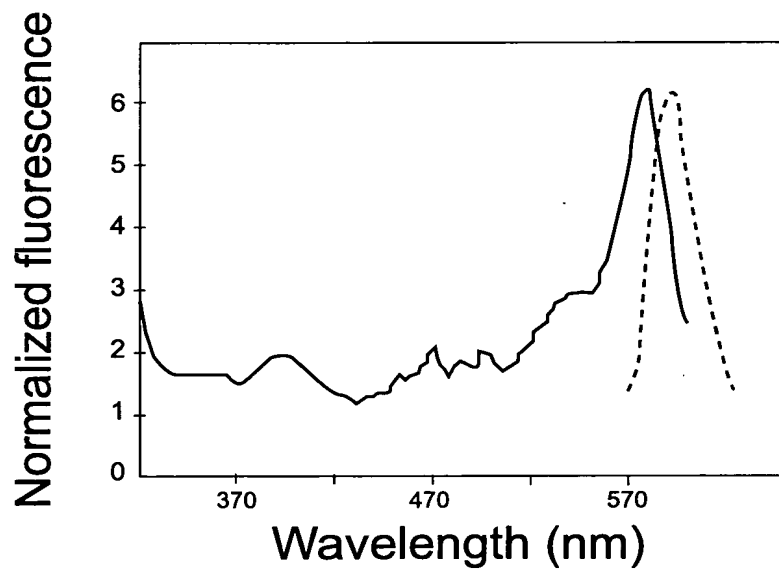


Fig. 13B

15/16

Relative absorbance

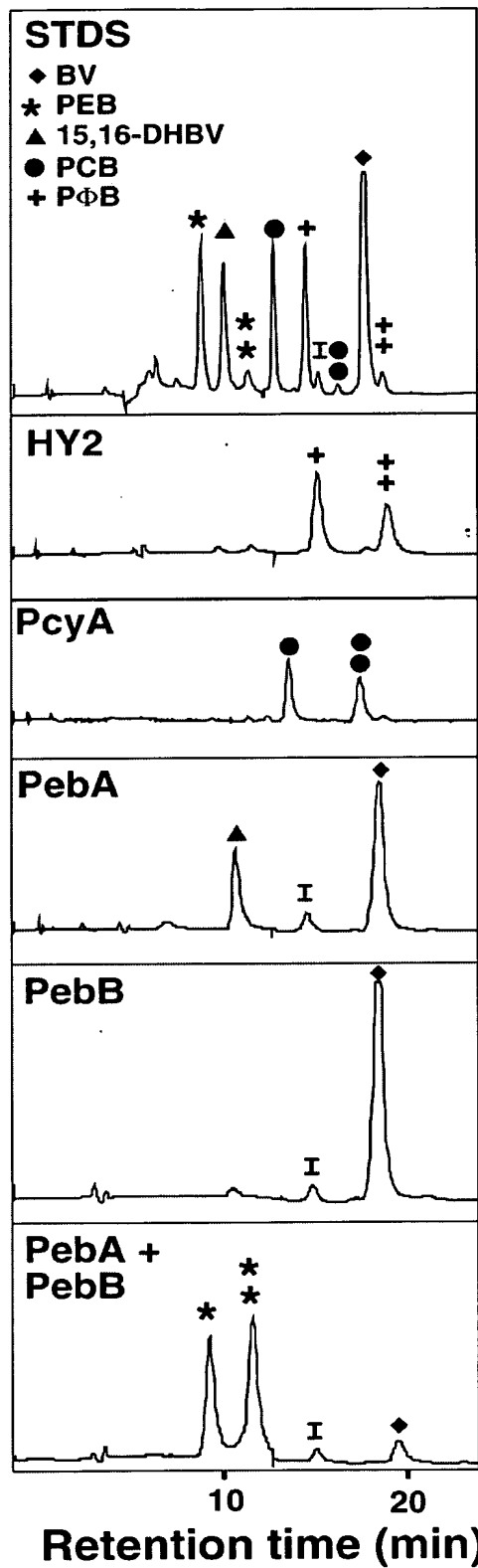


Fig. 14

16/16

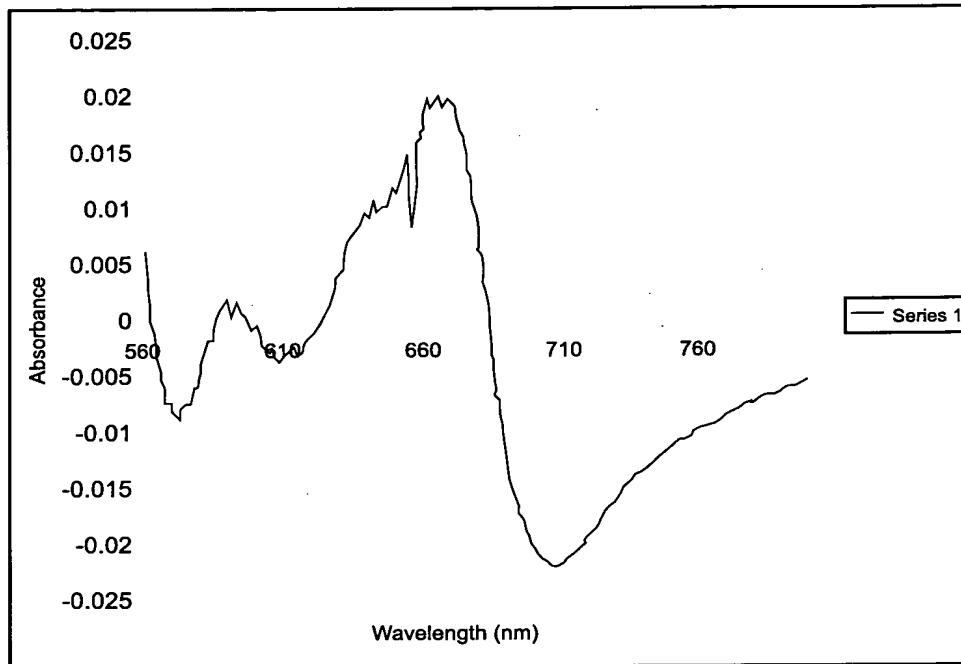


Fig. 15

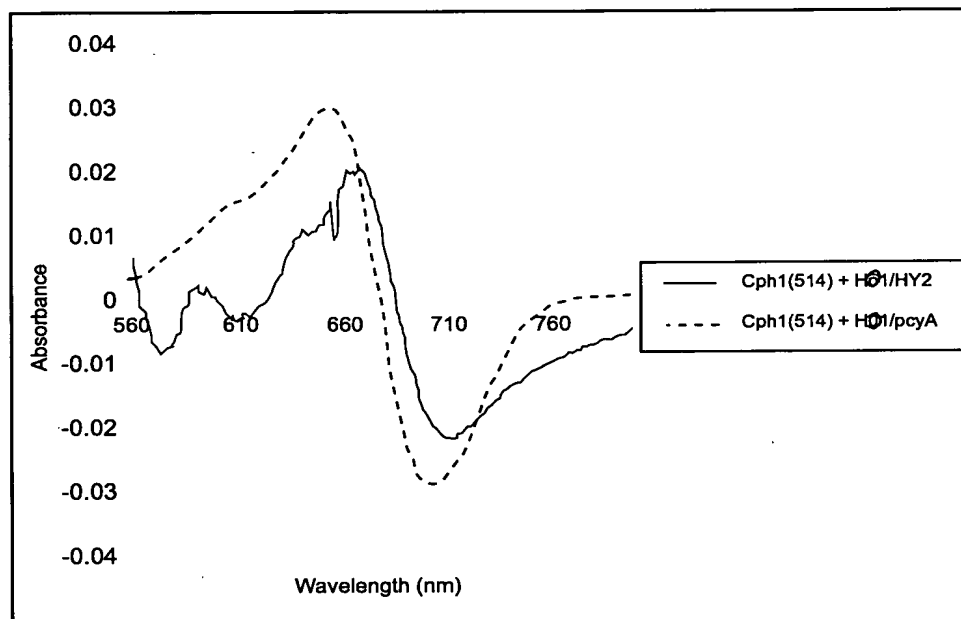


Fig. 16